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**Structural Studies of *E. Coli* Cysteinyl-tRNA Synthetase**

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Beamline(s): X12C

**Introduction:** Aminoacyl-tRNA synthetases are a class of enzymes responsible for the correct attachment of amino acids to their cognate tRNAs which then transfer the amino acids to a growing peptide chain on the ribosome. Cysteinyl-tRNA synthetase (CysRS) specifically attached cysteine to its cognate tRNA. The crystal structure of CysRS has been solved to 2.3Å resolution (unpublished data). X-ray crystallography is an important tool for understanding structure-function relationships of proteins.

**Methods and Materials:** Crystals of CysRS were grown in the presence of cysteine and ATP from a solution containing PEG-8000 as the precipitating agent. Crystals reached maximum dimensions of 0.2 x 0.2 x 0.05mm in approximately 3 weeks. Crystals were soaked with ligands cysteine and ATP for approximately 30 minutes prior to data collection. A complete dataset was collected at beamline X12C and data were processed using MOSFLM [3] and SCALA [2] refined against the unliganded CysRS structure using CNS [1].

**Results:** Fo-fo maps showed clear density for the ligand cysteine. The substrate was built into the model and the structure is currently being analyzed.

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**References:**

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